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0321

## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/084,507  
Source: OIPE  
Date Processed by STIC: 3-14-02

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:  
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202  
Or  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

## Raw Sequence Listing Error Summary .

### ERROR DETECTED      SUGGESTED CORRECTION

SERIAL NUMBER: 10/084,587

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line. This may occur if your file  
     Wrapped Aminos      was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will  
                                  prevent "wrapping."
  
- 2      Invalid Line Length      The rules require that a line not exceed 72 characters in length. This includes white spaces.
  
- 3      Misaligned Amino      The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers;  
     Numbering      use space characters, instead.
  
- 4      Non-ASCII      The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please  
                          ensure your subsequent submission is saved in ASCII text.
  
- 5      Variable Length      Sequence(s)      contain n's or Xaa's representing more than one residue. Per Sequence Rules,  
                                  each n or Xaa can only represent a single residue. Please present the maximum number of each  
                                  residue having variable length and indicate in the <220>-<223> section that some may be missing.
  
- 6      PatentIn 2.0      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid  
     "bug"      sequences(s)     . Normally, PatentIn would automatically generate this section from the  
                          previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to  
                          the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for  
                          Artificial or Unknown sequences.
  
- 7      Skipped Sequences      Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
     (OLD RULES)      (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                          (i)      SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                          (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                          This sequence is intentionally skipped  
  
                          Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
  
- 8      Skipped Sequences      Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence.  
     (NEW RULES)      <210> sequence id number  
                          <400> sequence id number  
                          000
  
- 9 ✓      Use of n's or Xaa's      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
     (NEW RULES)      Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
                          In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
  
- 10      Invalid <213>      Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or  
     Response      scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or  
                          is Artificial Sequence
  
- 11      Use of <220>      Sequence(s)      missing the <220> "Feature" and associated numeric identifiers and responses.  
                          Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or  
                          "Unknown." Please explain source of genetic material in <220> to <223> section.  
                          (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
  
- 12      PatentIn 2.0      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,  
     "bug"      resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence  
                          listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

Does Not Comply  
Corrected Diskette Needed



OIPE

## RAW SEQUENCE LISTING

DATE: 03/14/2002

PATENT APPLICATION: US/10/084,507

TIME: 12:24:35

Input Set : A:\10807400023.txt

Output Set: N:\CRF3\03142002\J084507.raw

```

3 <110> APPLICANT: MUNROE, Donald G.
4     KAMBOJ, Rajender
5     PETERS, Diana
6     KOOSHESH, Fatemeh
7     VYAS, Tejal B.
8     GUPTA, Ashwani K.
10 <120> TITLE OF INVENTION: IDENTIFICATION OF LYSOLIPID RECEPTORS INVOLVED IN
11     INFLAMMATORY RESPONSE
13 <130> FILE REFERENCE: 8074-8021
C--> 15 <140> CURRENT APPLICATION NUMBER: US/10/084,507
C--> 16 <141> CURRENT FILING DATE: 2002-02-28
18 <150> PRIOR APPLICATION NUMBER: 60/109,885
19 <151> PRIOR FILING DATE: 1998-11-25
21 <150> PRIOR APPLICATION NUMBER: 60/080,610
22 <151> PRIOR FILING DATE: 1998-04-03
24 <150> PRIOR APPLICATION NUMBER: 60/070,185
25 <151> PRIOR FILING DATE: 1997-12-30
27 <160> NUMBER OF SEQ ID NOS: 25
29 <170> SOFTWARE: PatentIn Ver. 2.1

```

## ERRORED SEQUENCES

```

334 <210> SEQ ID NO: 17
335 <211> LENGTH: 353
336 <212> TYPE: PRT
337 <213> ORGANISM: Homo sapiens
339 <400> SEQUENCE: 17
340 Met Gly Ser Leu Tyr Ser Glu Tyr Leu Asn Pro Asn Lys Val Gln Glu
341   1           5           10           15
343 His Tyr Asn Tyr Thr Lys Glu Thr Leu Glu Thr Gln Glu Thr Thr Ser
344           20           25           30
346 Arg Gln Val Ala Ser Ala Phe Ile Val Ile Leu Cys Cys Ala Ile Val
347           35           40           45
349 Val Glu Asn Leu Leu Val Leu Ile Ala Val Ala Arg Asn Ser Lys Phe
350           50           55           60
352 His Ser Ala Met Tyr Leu Phe Leu Gly Asn Leu Ala Ala Ser Asp Leu
353   65           70           75           80
355 Leu Ala Gly Val Ala Phe Val Ala Asn Thr Leu Leu Ser Gly Ser Val
356           85           90           95
358 Thr Leu Arg Leu Thr Pro Val Gln Trp Phe Ala Arg Glu Gly Ser Ala
359           100          105          110
361 Phe Ile Thr Leu Ser Ala Ser Val Phe Ser Leu Leu Ala Ile Ala Ile

```

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/084,507

DATE: 03/14/2002

TIME: 12:24:35

Input Set : A:\10807400023.txt

Output Set: N:\CRF3\03142002\J084507.raw

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362      115      120      125
364 Glu Arg His Val Ala Ile Ala Lys Val Lys Leu Tyr Gly Ser Asp Lys
365      130      135      140
367 Ser Cys Arg Met Leu Leu Leu Ile Gly Ala Ser Trp Leu Ile Ser Leu
368 145      150      155      160
370 Val Leu Gly Gly Leu Pro Ile Leu Gly Trp Asn Cys Leu Gly His Leu
371      165      170      175
373 Glu Ala Cys Ser Thr Val Leu Pro Leu Tyr Ala Lys His Tyr Val Leu
374      180      185      190
376 Cys Val Val Thr Ile Phe Ser Ile Ile Leu Leu Ala Ile Val Ala Leu
377      195      200      205
379 Tyr Val Arg Ile Tyr Cys Val Val Arg Ser Ser His Ala Asp Met Ala
380      210      215      220
382 Ala Pro Gln Thr Leu Ala Leu Leu Lys Thr Val Thr Ile Val Leu Gly
383 225      230      235      240
385 Val Phe Ile Val Cys Trp Leu Pro Ala Phe Ser Ile Leu Leu Leu Asp
386      245      250      255
388 Tyr Ala Cys Pro Val His Ser Cys Pro Ile Leu Tyr Lys Ala His Tyr
389      260      265      270
E--> 391 Xaa Phe Ala Val Ser Thr Leu Asn Ser Leu Leu Asn Pro Val Ile Tyr
392      275      280      285
394 Thr Trp Arg Ser Arg Asp Leu Arg Arg Glu Val Leu Arg Pro Leu Gln
395      290      295      300
397 Cys Trp Arg Pro Gly Val Gly Val Gln Gly Arg Arg Arg Gly Gly Thr
398 305      310      315      320
400 Pro Gly His His Leu Leu Pro Leu Arg Ser Ser Ser Ser Leu Glu Arg
401      325      330      335
403 Gly Met His Met Pro Thr Ser Pro Thr Phe Leu Glu Gly Asn Thr Val
404      340      345      350
406 Val
411 <210> SEQ ID NO: 18
412 <211> LENGTH: 1170
413 <212> TYPE: DNA
414 <213> ORGANISM: Homo sapiens
416 <400> SEQUENCE: 18
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419 cctctgctgg agggcggtcc accggagccg gaagtagcag taggagacaa cgcggtaaca 180
420 ccaccttttg gaagaccacg agtaacgcca ccgggctttg tcgttcaagg tgagccgtta 240
421 catggacaaa gaccggttgg accggcggag gctagatgac cgtccgcacc ggaagcatcg 300
422 gttatggaac gagagaccga gacagtgcga ctccgactgc ggacacgtca ccaaaccggc 360
423 cctcccagaga cggaagtagt gcgagagccg gagacagaag tcggaggacc ggtagcggta 420
424 actcgcggtg caccggtaac ggttccagtt cgacataccg tcgctgttct cgacggcgta 480
425 cgaagacgag tagccccgga gcaccgagta gagcgaccag gagccaccgg acgggtagga 540
426 accgaccttg acggaccggg tggagctccg gacgaggtga caggacggag agatgcggtt 600
427 cgtaatacac gacacgcacc aetggtagaa gaggtagtag gacaaccggt agcaccggga 660
428 catgcacgcg tagatgacgc accaggcgag ttcggtgcga ctgtaccggc ggggctctg 720
429 cgatcgggac gagttctgcc agtggttagca cgatccgcag aaatagcaga cgaccgacgg 780
430 gcggaagtcg taggaggaag acctgatacg gacagggcag gtgaggacgg gctaggagat 840

```

All 'Xaa' must  
have feature with  
numeric identifiers  
42207 - 42237.  
See item # 9 on  
ERROR Summary  
SHEET.

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/084,507

DATE: 03/14/2002

TIME: 12:24:35

Input Set : A:\10807400023.txt

Output Set: N:\CRF3\03142002\J084507.raw

431 gtttcgggtg atgraaaagc ggcagaggtg ggacttaagg gacgagttgg ggcagtagat 900  
 E--> 432 gtgcaccgcg tcggccctgg acgcccct ccacgaagcc ggcgacgta cgaccgccg 960  
 433 cccccacccc cagtttctg cctccgcccc gccctggggc ccggtggtgg aggacggtga 1020  
 434 ggcgtcgagg tcgagggacc tctccccgta cgtgtacggg tgcagtgggt gaaaagacct 1080  
 435 ccggttggtc caccagactc ccacccccac ctggttggtg gtccggtccc gtatcccaa 1140  
 436 gtacctttcc ggtgaccac tggggtttat 1170  
 742 <210> SEQ ID NO: 25  
 743 <211> LENGTH: 1056  
 744 <212> TYPE: DNA  
 745 <213> ORGANISM: Homo sapiens  
 747 <400> SEQUENCE: 25  
 748 taccagtagt acccggtcac gatgatgtg ctctggtagc cgaagaagat attggtgtca 60  
 749 ccgtttctcg agtcgaggtg gaccgccggg ttctacacc agcaccaccg tgaccgccgac 120  
 750 tggcagtcgc acgaccacga cgactggtta gacgaccagt atcgtcggtg gcggaggttg 180  
 751 gcggcgaagg tggtcgggta gatgatggac gagccgttag accggcgccg actggagaag 240  
 752 cgcccgaccc ggatggagaa ggagtacaag gtgtgaccag gggcgtgtcg ggctgaaagt 300  
 753 gaactcccga ccaaggacgc cgtcccgaac gacctgtgtt cggagtgcg cagccaccgg 360  
 754 tgtgacgacc ggtagcggca cctcgccgtg gcgtcacact accggcacgt cgacgtgtcg 420  
 755 gcggacgggg caccggcgca ccagtacgag taacaccgcg acaccaccg acgggaccg 480  
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 758 aaggacgagt accaccgaca catgtggcg taaaagaaga tgcacgcgc cgctcacgtc 660  
 759 gcgtaccgtc tcgtacagtc gacggtgggg gcgatggctc tctggtgcga gtcggaccag 720  
 760 ttctgacaac agtagtagga ccccgcaag caccagacga cctgtggtcc ggtccaccat 780  
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 765 ctcttgccgg tgggtgacta cctgaggtgg gaaatc 1056  
 E--> 771 2

remove extra g material at end of file.

## VERIFICATION SUMMARY

DATE: 03/14/2002

PATENT APPLICATION: US/10/084,507

TIME: 12:24:36

Input Set : A:\10807400023.txt

Output Set: N:\CRF3\03142002\J084507.raw

L:15 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:308 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:16  
L:308 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16  
L:391 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:17  
L:432 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:18  
L:771 M:254 E: No. of Bases conflict, LENGTH:Input:2 Counted:1056 SEQ:25